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1

SEQUENCE LISTING

<110> SEIKAGAKU CORPORATION

<120> Method for detecting cancer

<130> F20041104109

<150> JP 2003-185696

<151> 2003-6-27

<160> 5

<170> PatentIn version 3.1

<210> 1

<211> 1292

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (181) .. (1200)

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agagctaaca tttttggtga ggaaagcact gcaggagcag gctggcacag agaagaggac 180

atg cgg aag gag ctc cag ctc tcc ctg tca gtc acc ttg ctg ctt gtc 228

Met Arg Lys Glu Leu Gln Leu Ser Leu Ser Val Thr Leu Leu Leu Val

1 5 10 15

tgt ggc ttc ctc tac cag ttc acc ctg aag tcc agc tgc ctc ttc tgt 276

Cys Gly Phe Leu Tyr Gln Phe Thr Leu Lys Ser Ser Cys Leu Phe Cys

20 25 30

ttg cct tot ttc aag tcc cac cag ggg ctg gaa gcc ctc ctg agc cac 324

Leu Pro Ser Phe Lys Ser His Gln Gly Leu Glu Ala Leu Leu Ser His

35 40 45

aga cgt ggc att gtg ttt cta gag acc tca gag aga atg gag cca ccc 372

Arg Arg Gly Ile Val Phe Leu Glu Thr Ser Glu Arg Met Glu Pro Pro

50 55 60

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2

cat ttg gtc tcc tgt tcc gta gag tct gct gcc aag att tat cct gag	420
His Leu Val Ser Cys Ser Val Glu Ser Ala Ala Lys Ile Tyr Pro Glu	
65 70 75 80	
tgg cct gtg gtg ttc ttt atg aag ggt ctt act gat tcc aca ccg atg	468
Trp Pro Val Val Phe Phe Met Lys Gly Leu Thr Asp Ser Thr Pro Met	
85 90 95	
ccc tca aac tcc aca tac cca gct ttt tcc ttc ctg tca gca ata gac	516
Pro Ser Asn Ser Thr Tyr Pro Ala Phe Ser Phe Leu Ser Ala Ile Asp	
100 105 110	
aac gtt ttc ctc ttc cct ttg gat atg aaa agg ctg ctt gaa gac aca	564
Asn Val Phe Leu Phe Pro Leu Asp Met Lys Arg Leu Leu Glu Asp Thr	
115 120 125	
cca ttg ttt tca tgg tac aat caa atc aac gcc agc gca gag aga aac	612
Pro Leu Phe Ser Trp Tyr Asn Gln Ile Asn Ala Ser Ala Glu Arg Asn	
130 135 140	
tgg ctc cac atc agc tcg gat gca tcc cgc ctg gcc atc atc tgg aaa	660
Trp Leu His Ile Ser Ser Asp Ala Ser Arg Leu Ala Ile Ile Trp Lys	
145 150 155 160	
tac ggt ggc atc tac atg gac acc gat gtc atc tcc atc agg ccc atc	708
Tyr Gly Gly Ile Tyr Met Asp Thr Asp Val Ile Ser Ile Arg Pro Ile	
165 170 175	
cct gag gag aac ttt ttg gct gcg cag gct tct cgg tac tct agt aat	756
Pro Glu Glu Asn Phe Leu Ala Ala Gln Ala Ser Arg Tyr Ser Ser Asn	
180 185 190	
gga ata ttt ggg ttc ctc ccc cac cac ccc ttt ttg tgg gaa tgc atg	804
Gly Ile Phe Gly Phe Leu Pro His His Pro Phe Leu Trp Glu Cys Met	
195 200 205	
gaa aac ttt gtt gaa cac tat aat tca gcc att tgg ggc aac caa gcc	852
Glu Asn Phe Val Glu His Tyr Asn Ser Ala Ile Trp Gly Asn Gln Gly	
210 215 220	
cct gag ttg atg aca agg atg ttg agg gta tgg tgt aaa ctt gaa gac	900
Pro Glu Leu Met Thr Arg Met Leu Arg Val Trp Cys Lys Leu Glu Asp	
225 230 235 240	
ttc cag gag gtg agc gac ctc agg tgt ctg aac ata tcc ttc tta cac	948
Phe Gln Glu Val Ser Asp Leu Arg Cys Leu Asn Ile Ser Phe Leu His	
245 250 255	

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3

ccc caa aga ttt tac ccc atc tcc tat cga gag tgg agg cgc tac tat 996
 Pro Gln Arg Phe Tyr Pro Ile Ser Tyr Arg Glu Trp Arg Arg Tyr Tyr
 260 265 270

gaa gtg tgg gat aca gag cca agc ttc aat gtc tct tat gcc ctg cat 1044
 Glu Val Trp Asp Thr Glu Pro Ser Phe Asn Val Ser Tyr Ala Leu His
 275 280 285

ttg tgg aac cac atg aac cag gag ggg cgg gct gtg att aga gga agc 1092
 Leu Trp Asn His Met Asn Gln Glu Gly Arg Ala Val Ile Arg Gly Ser
 290 295 300

aac aca ctg gtg gaa aat ctc tat cgc aag cac tgt ccc agg act tac 1140
 Asn Thr Leu Val Glu Asn Leu Tyr Arg Lys His Cys Pro Arg Thr Tyr
 305 310 315 320

agg gac ctg att aaa ggc cca gag ggg tca gtg act ggg gag ctg ggt 1188
 Arg Asp Leu Ile Lys Gly Pro Glu Gly Ser Val Thr Gly Glu Leu Gly
 325 330 335

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 Leu Pro Ser Phe Lys Ser His Gln Gly Leu Glu Ala Leu Leu Ser His
 35 40 45
 Arg Arg Gly Ile Val Phe Leu Glu Thr Ser Glu Arg Met Glu Pro Pro
 50 55 60
 His Leu Val Ser Cys Ser Val Glu Ser Ala Ala Lys Ile Tyr Pro Glu
 65 70 75 80
 Trp Pro Val Val Phe Phe Met Lys Gly Leu Thr Asp Ser Thr Pro Met
 85 90 95
 Pro Ser Asn Ser Thr Tyr Pro Ala Phe Ser Phe Leu Ser Ala Ile Asp
 100 105 110

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Asn Val Phe	Leu Phe Pro Leu Asp Met Lys Arg Leu Leu Glu Asp Thr
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Pro Leu Phe	Ser Trp Tyr Asn Gln Ile Asn Ala Ser Ala Glu Arg Asn
130	135 140
Trp Leu His	Ile Ser Ser Asp Ala Ser Arg Leu Ala Ile Ile Trp Lys
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Tyr Gly Gly	Ile Tyr Met Asp Thr Asp Val Ile Ser Ile Arg Pro Ile
	165 170 175
Pro Glu Glu	Asn Phe Leu Ala Ala Gln Ala Ser Arg Tyr Ser Ser Asn
	180 185 190
Gly Ile Phe	Gly Phe Leu Pro His His Pro Phe Leu Trp Glu Cys Met
195	200 205
Glu Asn Phe	Val Glu His Tyr Asn Ser Ala Ile Trp Gly Asn Gln Gly
210	215 220
Pro Glu Leu	Met Thr Arg Met Leu Arg Val Trp Cys Lys Leu Glu Asp
225	230 235 240
Phe Gln Glu	Val Ser Asp Leu Arg Cys Leu Asn Ile Ser Phe Leu His
	245 250 255
Pro Gln Arg	Phe Tyr Pro Ile Ser Tyr Arg Glu Trp Arg Arg Tyr Tyr
	260 265 270
Glu Val Trp	Asp Thr Glu Pro Ser Phe Asn Val Ser Tyr Ala Leu His
275	280 285
Leu Trp Asn	His Met Asn Gln Glu Gly Arg Ala Val Ile Arg Gly Ser
290	295 300
Asn Thr Leu	Val Glu Asn Leu Tyr Arg Lys His Cys Pro Arg Thr Tyr
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Pro Gly Asn	Lys
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26

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